

Correlation of a Subset of the pLC Plasmids to the Physical Map of *Escherichia coli* K-12

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INTRODUCTION

The pLC plasmid collection was constructed by Clarke and Carbon (3, 4) and consists of 2,200 strains that harbor hybrid *Escherichia coli* K-12-ColE1 plasmids (pLC plasmids). Each hybrid DNA circle contains a random piece of *E. coli* K-12 chromosomal DNA that was mechanically sheared to an average size of 14 kb and was ligated to ColE1 DNA by the AT-tailing method. The plasmids can be transferred to F⁻ strains by the F-mediated conjugative system. This provides a convenient screening procedure for the ability of a cloned segment of DNA to suppress or complement *E. coli* mutations. A bank of this size is statistically expected to cover 99% of the entire chromosomal DNA. However, the map positions of most pLC plasmids have not been identified. In the first edition of the bank, Clarke and Carbon selected 173 specific clones from the bank based on suppression or complementation tests using mutations in well-characterized genes (5). The latest edition of the gene-protein index of "Clarke & Carbon's collection" presented map locations of 310 species of pLC plasmids by either complementation, expression of proteins previously identified, or hybridization to known genes (18). The total region covered by them was approximately 10% of the entire chromosome.

Kohara et al. established the bank of 3,400 overlapping lambda phage clones containing segments of the *E. coli* chromosome and constructed a 4,700-kb integrated restriction map for eight six-base-recognizing enzymes (12). Recently, about 500 gene loci were located on the physical map of *E. coli* after a systematically survey of the EMBL DNA data base and literature containing *E. coli* restriction data (11, 15).

In the work reviewed in this paper, 518 pLC plasmids were located on the physical map by plaque hybridization to clones of the *E. coli* ordered clone bank. The plasmids we analyzed covered approximately half of the entire map of *E. coli*.

The physical mapping of the pLC plasmids reported here will increase the use of this tool for genetic analyses and gene cloning in *E. coli*.

MATERIALS AND METHODS

Bacterial and Phage Strains

The Clarke & Carbon collection (3, 4) was kindly provided by K. Ueda, Kyoto University. For plaque hybridization assays, the miniset (11) of *E. coli* ordered clone bank was used.

Plaque Hybridization

The phage clones of the miniset of the *E. coli* ordered clone bank (476 phage clones, six microtiter plates) were transferred from the master plates to lawns of strain W3110 on LB plates as described previously (12) with slight modifications. The resulting plaques were replicated onto strips of nylon membrane (11.5 by 8 cm; Nihon Pall-BNNG3R). From one plate, 10 replicas were made. The membranes were immediately immersed in a denaturing solution (0.5 M NaOH, 1.5 M NaCl) for 1 min and then in a neutralizing solution (1 M Tris HCl [pH 7.0], 1.5 M NaCl) for 5 min, and they were then washed in 2× SSC (1× SSC is 0.15 M NaCl plus 0.015 M sodium citrate). After being dried at room temperature, the membranes were baked at 80°C for 2 h and stored in a desiccator until use.

The probe DNA was denatured as follows: 30 ng to 1 µg of pLC plasmid DNA was denatured in 0.5 N NaOH at 95°C for 3 min, immediately cooled on ice, and neutralized with 1/10 vol of 5 M HCl-0.5 M Tris HCl (pH 8.0). The linearized and fragmented (about 2,300 nucleotides) DNA was precipitated with ethanol and was then labeled by randomly primed incorporation of digoxigenin-labeled dUTP. The nylon membrane was subjected to hybridization to the probe DNA, and the hybridized probe was detected by the enzyme-linked immunoassay and subsequent enzyme-catalyzed color reaction by using the Nonradioactive DNA-Labeling and Detection Kit (Boehringer Mannheim).

CORRELATION OF pLC PLASMIDS TO THE *E. COLI* MAP

To arrange pLC plasmids on the genetic map of *E. coli*, we examined each pLC plasmid by plaque hybridization to the *E. coli* ordered clone bank as described in Materials and Methods. Of the 2,200 pLC plasmids in the Clarke and Carbon library, we used 518 for the hybridization tests. Of

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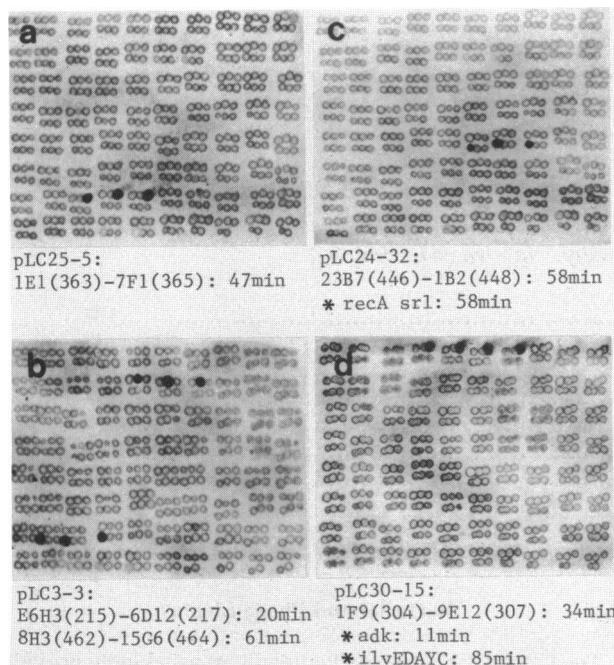


FIG. 1. Examples of plaque hybridization. Six packed arrays of phage clones in 80 blocks (miniset of *E. coli* ordered clone bank) were adsorbed onto strips of nylon membrane and hybridized with probe DNAs pLC25-5 (a), pLC3-3 (b), pLC24-32 (c), and pLC30-15 (d), as described in Materials and Methods. The black spots represent positive results, i.e., coloration of the hybridized clone DNA. The clone numbers of the positive spots are indicated along with their approximate map location (minutes). Genes identified by Phillips et al. (18) are also indicated, along with their map position.

these, 87 were randomly selected and the other 431 were the plasmids that complemented our collection of 282 *fts* mutants of *E. coli* which form filaments at nonpermissive temperatures. These *fts* mutations turned out to map at more than 50 different loci scattered all over the *E. coli* chromosome (16). Examples of the results of hybridization experiments are shown in Fig. 1. The chromosomal locations of 297 clones of the Clarke and Carbon library were newly determined in the present study. Of 518 plasmids tested, 180 plasmids gave results that agreed with those reported in a previous paper on the gene protein index (18). An example of such a result is shown in Fig. 1c. On the other hand, 41 plasmids gave entirely different map positions from those previously reported (18) (Fig. 1d). One possibility is that the discrepancy is due to the presence of multicopy suppressor genes which apparently complement mutations when the gene is present in multiple copies in a cell (20). Different map locations may be deduced in such cases by genetic versus physical analyses. Of the 41 pLC plasmids that mapped at different positions from those previously reported, 39 hy-

bridized to two or more lambda clones which are adjacent or overlap on the *E. coli* chromosome. It is therefore unlikely that the discrepancies are due to any possible cross-contamination of our phage stocks.

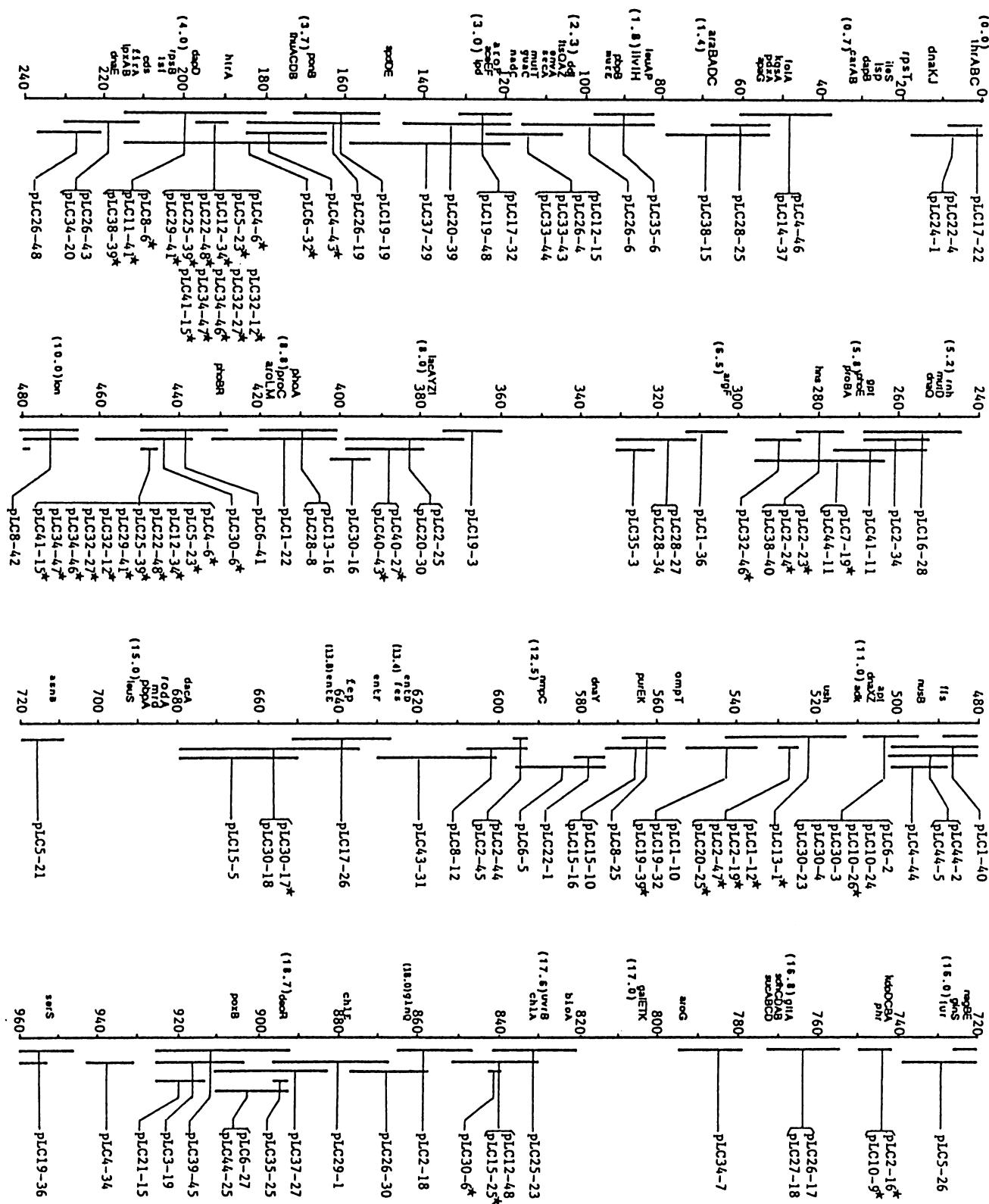
Most of the pLC plasmids hybridized to a few adjacent clones of the *E. coli* ordered clone library (Fig. 1a, c, and d). Some plasmids hybridized to two groups of clones (Fig. 1b) which were located at different positions. This might be due to general repeated sequences such as insertion (IS) elements (2), palindromic units (8), repetitive extragenic palindromic sequences (7), or tRNA genes (13). Furthermore, we have found that the *E. coli* K-12 chromosome carries a novel repeated sequence which has been mapped at 4, 9, 28, and 59 min (15a). Some pLC plasmids, pLC4-6 and pLC5-23 for example, carry this repeated sequence. Additional repeated sequences might exist in *E. coli*. Another possible explanation for this would be provided by the electron-microscopic observations reported in our previous papers (17, 20), which showed that two plasmids of distinct sizes were found in certain strains, for example JA200(pLC4-16) and JA200 (pLC4-43). The third possibility is that two different pieces of chromosomal DNA have been ligated into one molecule of the ColE1 vector.

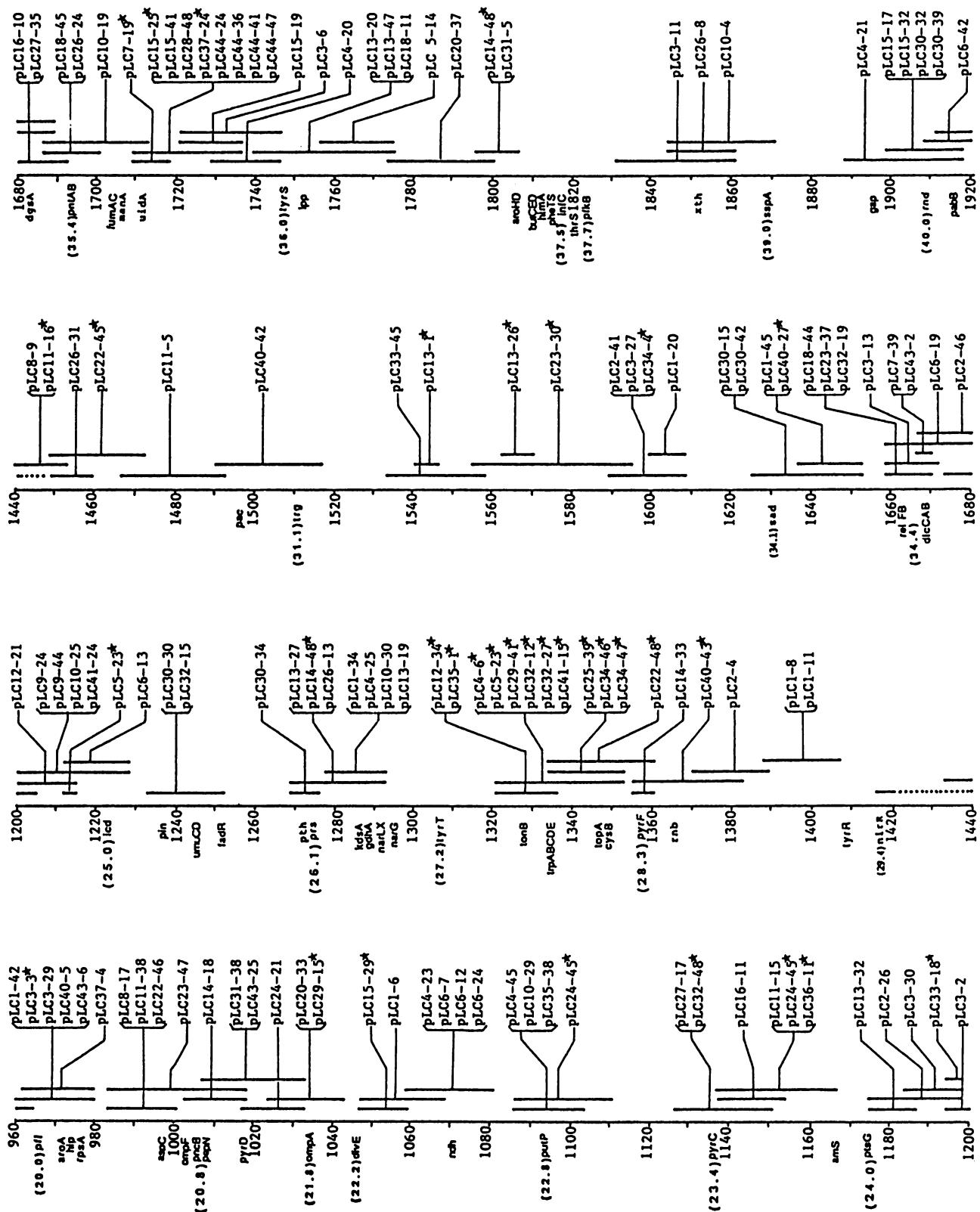
The total number of plasmids which we analyzed by plaque hybridization is 518, and the regions corresponding to each plasmid are indicated by bars on the physical map of *E. coli* chromosome shown in Fig. 2. The total length of chromosome covered with the bars is 83%. However, the bars simply indicate the maximal length which does not overlap with the adjacent lambda clones which did not hybridize to the plasmids. Therefore, it is difficult to accurately estimate the total length of the chromosomal regions which are covered by these 518 plasmids. We have previously determined the molecular size of the chromosomal moiety of 11 pLC plasmids by measuring their contour length in electron microscope (17, 20) and obtained an average value corresponding to 12 kb. The average length of the bars for these 11 pLC plasmids in Fig. 2 corresponds to 23 kb. Taking this observation into account, we would roughly estimate that approximately half of the entire *E. coli* chromosome is actually covered by the 518 plasmids used in this study.

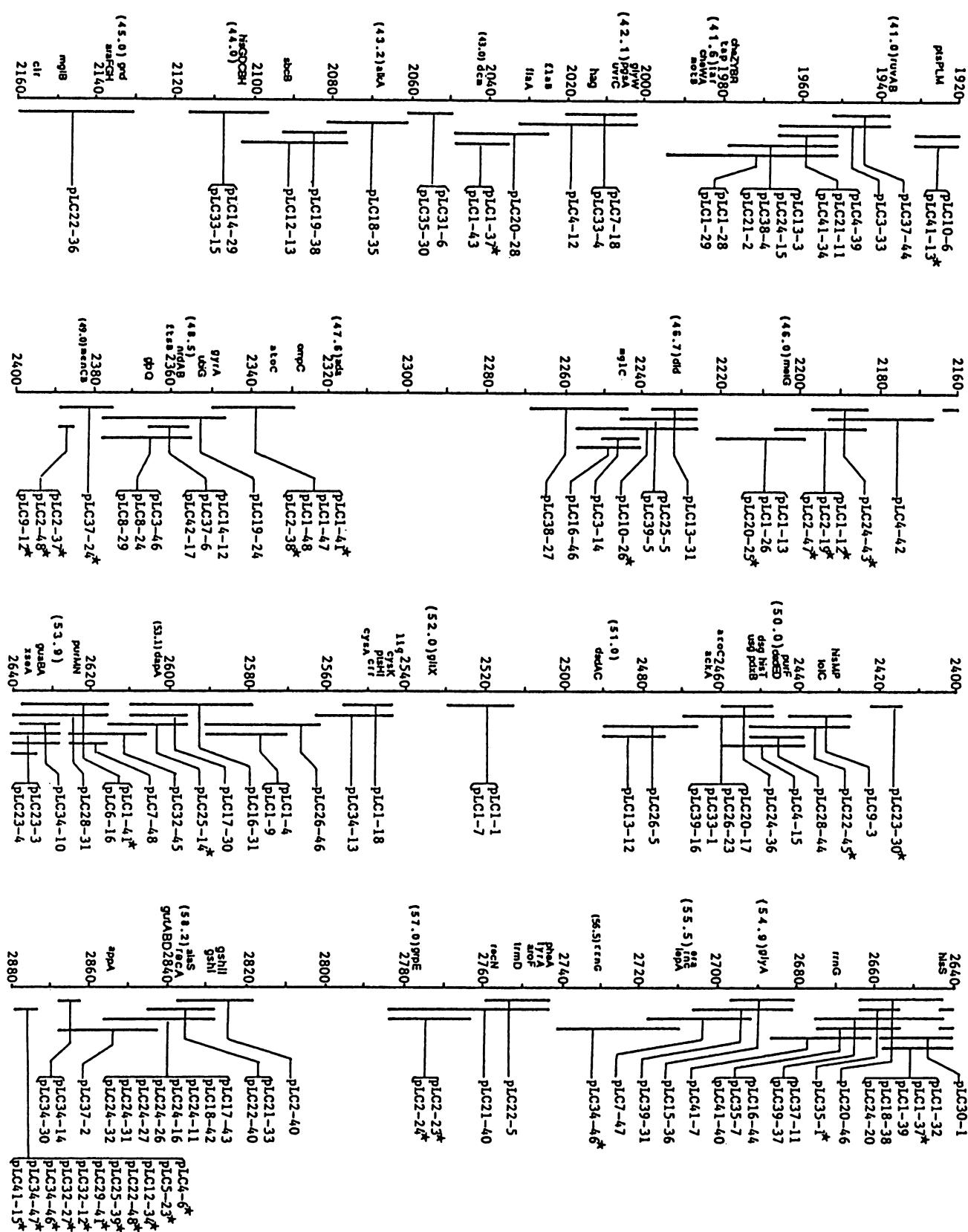
A correlation between pLC plasmids and the *E. coli* ordered clones is listed in Table 1. In this table, all the miniset clones of the *E. coli* ordered clone bank which hybridized to each pLC plasmid are listed along with their approximate map positions. Further identification of the remaining pLC plasmids by plaque hybridization is in progress. Whether the entire pLC plasmid collection covers the whole *E. coli* genome has yet to be determined.

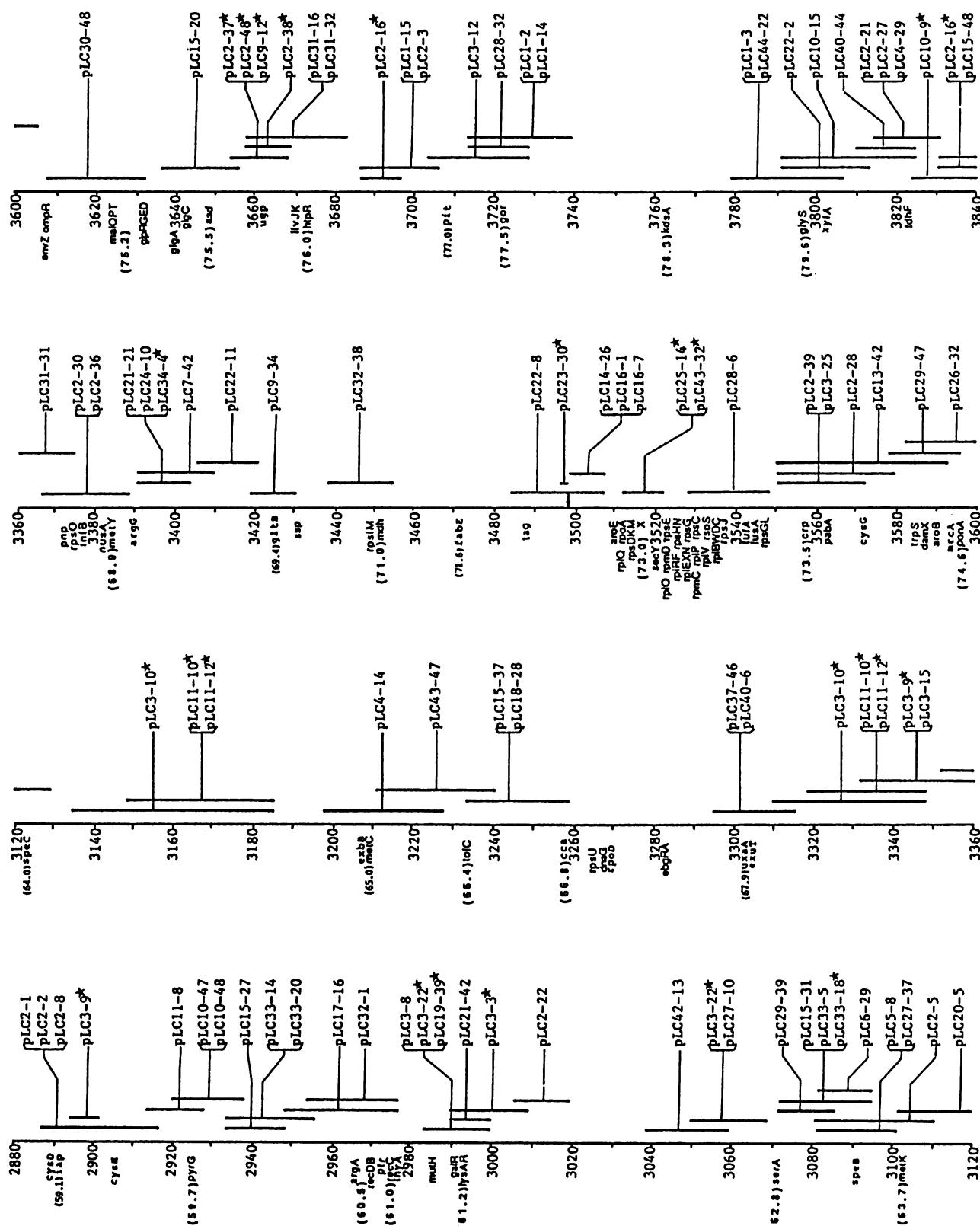
There is a possibility that some genes are not included in the 2,200 clones of the pLC plasmid collection because multicopy plasmids carrying certain genes could be deleterious to the cell. The use of other sets of cloned segments such as cosmid libraries (6, 10, 19) or the libraries made on F' single-copy plasmids (14) may alleviate this problem (18).

FIG. 2 Location of pLC plasmids on the physical map. The vertical bars show the DNA regions carried by pLC plasmids which hybridized to the various *E. coli* ordered clones. However, the ends of each bar have not been accurately determined. The bars simply indicate the maximal length which does not overlap with the adjacent lambda clones which did not hybridize to the plasmids. The pLC plasmids that hybridized to clones from more than one location are indicated by ★. To make a map which is compatible with the genetic map published by Bachmann (1) and with the plasmid map by Phillips et al. (18), the revised physical map of Médigue et al. (15) was used. Médigue et al. have restored the inversion in the strain W3110 used by Kohara et al. (i.e., inversion between *rrnD* and *rrnE* [9]) to its normal orientation and have located on it the sequenced genes available in the EMBL library. Some additional genes are from a previous paper by Kohara (11).









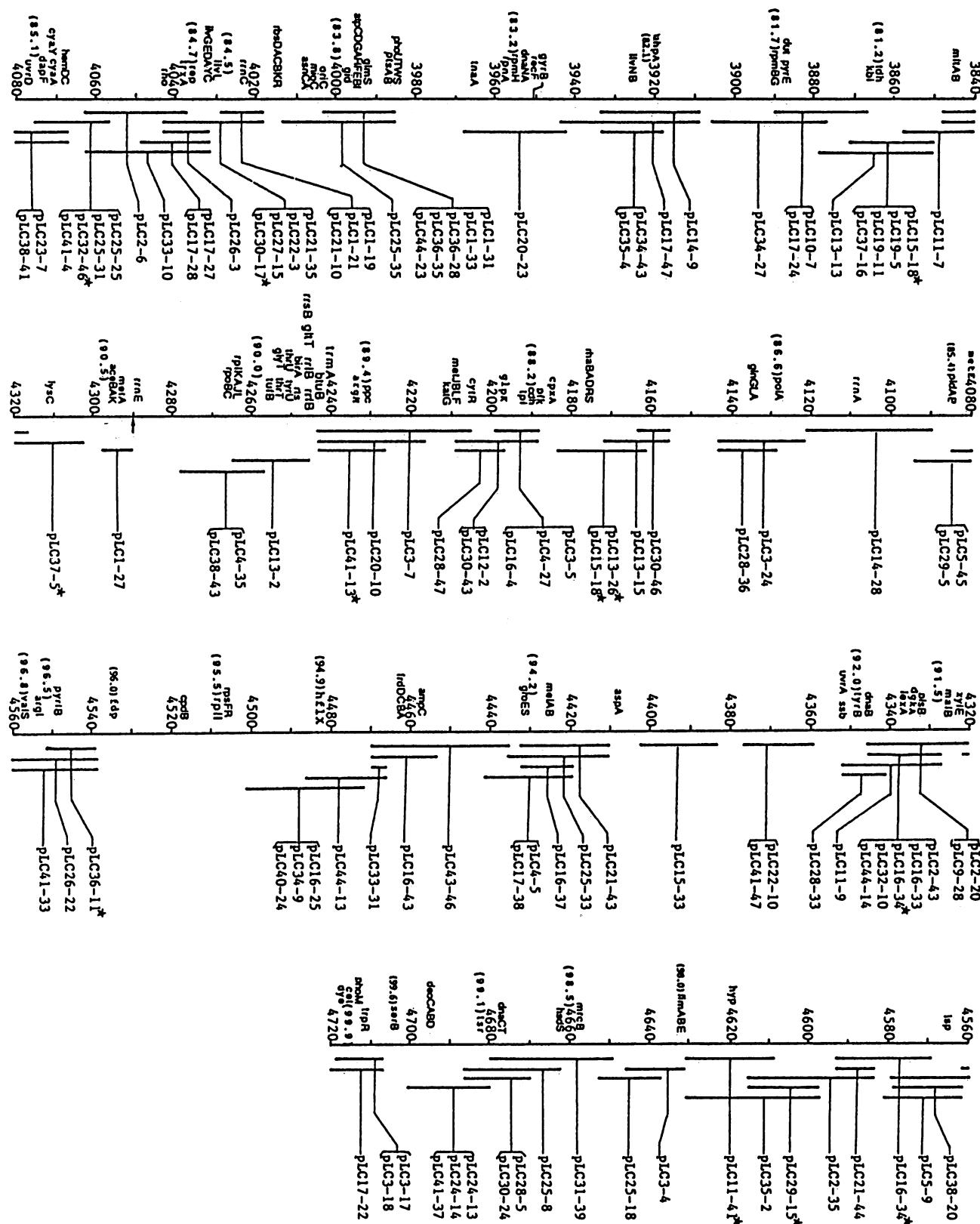


TABLE 1. Correlation between pLC and the *E. coli* ordered clones as determined by hybridization experiments

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c
1-1	52	10D3 (414), 12H4 (415), 4G10 (416)	2-26	25	E9G1 (236), 15A8 (237), E4C2 (238)
1-2	77	9G3 (606), 4D9 (607), 12E4 (608)	2-27	80	2C10 (577), 9B3 (578), 7C3 (579)
1-3	80	10C8 (580), 6F2 (601), 9F6 (602)	2-28	74	6F9 (623), 15C3 (624), 4C5 (625)
	*	<i>glyS dctA xyl</i> (80 min)	2-30	69	13A9 (518), 18H7 (520)
1-4	53	4E10 (421), 7A8 (422)	2-34	6	4A11 (126), 8F9 (127)
1-6	22	4H9 (224), 4H11 (225), 2F1 (226)	2-35	98	16H7S (661), 7G7 (662), 9H9 (663), 19H10 (664)
1-7	52	10D3 (414), 12H4 (415), 4G10 (416)	2-36	69	13A9 (518), 18H7 (520)
1-8	29	2D3 (258), 3H8 (259), 6B4 (260)	2-37	76	1B6 (613), 5B10 (614), 10F5 (615)
1-9	53	4E10 (421), 7A8 (422)		49	5H12 (380)
1-10	12	8E4 (155), 9E5 (156)		*	<i>livH livK</i> (76 min)
1-11	29	2D3 (258), 3H8 (259), 6B4 (260)	2-38	76	1B6 (613), 5B10 (614)
1-12	46	8F4 (359), 3E4 (360), 2B4 (361)		48	5A1 (374), 4F12 (375), E13A5 (376)
	11	7C12 (154)		*	<i>livH</i> (76 min)
1-13	46	3E4 (360), 2B4 (361), 17A4 (362)	2-39	74	15C3 (624), 4C5 (625)
	*	<i>deoD</i> (99 min)	2-40	58	8G10 (445), 23B7 (446)
1-14	77	9G3 (606), 4D9 (607), 12E4 (608)	2-41	33	22E3 (280), 6E8 (301), 2A9 (302)
1-15	77	6A4 (609), 10D10 (610), 5F2 (611)	2-43	92	1F8 (634), 12B4 (635), 1E4 (636)
1-18	52	12G2 (418), 5F7 (419)		*	<i>dgkA plsB</i> (92 min)
1-19	84	2E6 (557), 15D10 (558)	2-44	13	23E10 (160)
1-20	34	6E8 (301), 2A9 (302)	2-45	13	23E10 (160)
1-21	84	2E6 (557), 15D10 (558)	2-46	35	7E6 (309), 6F6 (310), E3F2 (311)
1-22	9	6E2 (141), 1A10 (142), 6A12 (143), 9G9 (144)	2-47	11	7C12 (154)
1-26	46	3E4 (360), 2B4 (361), 17A4 (362)		46	8F4 (359), 3E4 (360), 2B4 (361)
1-27	90	18C4 (629), 5F12 (630)	2-48	76	1B6 (613), 5B10 (614), 10F5 (615)
1-28	42	20H4 (337), 12C7 (338), 7F11 (339), 18A9 (340)		49	5H12 (380)
	*	<i>flaHG cheZYBR tap tar cheWA motBA</i> (41 min)	3-2	25	E4C2 (238), 7F9 (239)
1-29	42	20H4 (337), 12C7 (338), 7F11 (339), 18A9 (340)		*	<i>purB asuE icd</i> (25 min)
	*	<i>flaHG cheZYBR tap tar cheWA mot</i> (41 min)	3-3	20	E6H3 (215), 13E3 (216), 6D12 (217)
1-31	84	2A1 (560), 7A1 (561)		61	8H3 (462), 12H3 (463), 15G6 (464)
1-32	54	8E3 (427), 2D5 (428), 7F8 (429)	3-4	98	1D6 (666), 5G8 (667), 8H8 (668)
1-33	84	2A1 (560), 7A1 (561)	3-5	88	4H12 (539), 8B10 (540)
1-34	27	4D10 (247), 13H6 (248)	3-6	36	9A1 (315), 20B5 (316), 6F11 (317)
1-36	7	21C10 (131), 5E5 (132)	3-7	89	4G11 (535), 8H10 (536), 6D8 (537), 12E3 (538)
1-37	43	25D8 (344)	3-8	61	5A10 (461), 8H3 (462), 12H3 (463)
	54	8E3 (427), 2D5 (428), 7F8 (429)	3-9	59	6C8 (452), 9A10 (453)
1-39	54	8E3 (427), 2D5 (428), 7F8 (429)	3-10	68	6B5 (515), 20F4 (516), 16C4 (517)
1-40	10	3B6 (148), 7E2 (149), 19B7 (150), 8C4 (151)		64	1G7 (478), 21H2 (479), 3B2 (480), 8A5 (501), 2F9 (502)
1-41	48	5A1 (374), 4F12 (375), E13A5 (376)		68	21D1 (513), 8F8 (514), 6B5 (515), 20F4 (516)
	54	10H6 (425), 5A11 (426), 8E3 (427)	3-11	38	19B6 (325), 4F7 (326), 5E12 (327), 4B8 (328)
	*	<i>ftsB</i> (49 min)	3-12	77	4D9 (607), 12E4 (608), 6A4 (609)
	*	<i>purL</i> (55 min)	3-13	35	12E2 (308), 7B6 (309), 6F6 (310)
1-42	20	E6H3 (215), 13E3 (216), 6D12 (217)		*	<i>lsp</i> (1 min)
1-43	43	25D8 (344)	3-14	47	2B1 (364), 7F1 (365), 7H12 (366)
1-45	34	2H2 (305), 2B2 (306), 9E12 (307)		*	<i>mglBAC</i> (45 min)
1-47	48	5A1 (374), 4F12 (375), E13A5 (376)	3-15	68	6B5 (515), 20F4 (516), 16C4 (517)
1-48	48	5A1 (374), 4F12 (375), E13A5 (376)	3-17	100	12A4 (675), 15A5 (676)
2-1	59	1B5 (451), 6C8 (452), 9A10 (453), 1B3 (454)	3-18	100	12A4 (675), 15A5 (676)
2-2	59	1B5 (451), 6C8 (452), 9A10 (453), 1B3 (454)	3-19	19	5F4 (210), 4H6 (211)
2-3	77	6A4 (609), 10D10 (610), 5F2 (611)	3-22	61	5A10 (461), 8H3 (462), 12H3 (463)
2-4	29	E14F6 (256), 1C2 (257), 2D3 (258)		63	22H4 (468), 5E11 (469), 10B4 (470)
2-5	63	6C5 (472), 1H10 (473), 23G4S (474), 12C6 (475)		*	<i>dgkA plsB</i> (92 min)
	*	<i>speAB endA metK</i> (63 min)	3-24	87	9H1 (545), 10F1 (546), 8D12 (547), 10H11 (548)
2-6	85	10F4 (554), 7B1 (555), 2A8 (556)		*	<i>rha</i> (88 min)
2-8	59	1B5 (451), 6C8 (452), 9A10 (453), 1B3 (454)	3-25	74	15C3 (624), 4C5 (625)
2-16	16	3G6 (174)	3-27	33	22E3 (280), 6E8 (301), 2A9 (302)
	77	10D10 (610), 5F2 (611)	3-29	20	E6H3 (215), 13E3 (216), 6D12 (217)
	81	17G2 (576), 2C10 (577)		*	<i>pdxC aroA</i> (20 min)
2-18	18	1B4 (204), 10A8 (205), 4C6 (206)	3-30	25	15A8 (237), E4C2 (238)
2-19	11	7C12 (154)	3-33	41	19H3 (336), 20H4 (337)
	46	8F4 (359), 3E4 (360), 2B4 (361)		*	<i>edd zwf</i> (41 min)
2-20	92	7A4 (633), 1F8 (634), 12B4 (635), 1E4 (636)	3-46	49	20E7 (377), 22C4 (378), 4B4 (379)
	*	<i>dgkA plsB</i> (92 min)		*	<i>nrdB ftsB glpQT</i> (48 min)
2-21	80	2C10 (577), 9B3 (578), 7C3 (579)	4-5	94	8H1 (645), 5H2 (646), 21H11 (647), 5G7 (648)
2-22	62	15G6 (464), 10D8 (465)		*	<i>lysU cadA</i> (94 min)
2-23	6	8G4 (128), 5A5 (129)	4-6	28	14C4 (252), 4F1 (253), 13F9 (254)
	57	24G1 (440), 4C9 (441)		4	21C8 (119)
2-24	6	8G4 (128), 5A5 (129)		10	19F6 (146)
	57	24G1 (440), 4C9 (441)		59	25D2 (450)
2-25	8	10A6 (138), 7H10 (139), 8F10 (140)			

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TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c
	*	<i>trpBCDE topA cysB</i> (28 min)	6-42	40	6D1 (333), 12B3 (334), 15D5 (335)
4-12	42	16B12 (341), 4B9 (342), 3B3 (343)	7-18	42	16B12 (341), 4B9 (342)
	*	<i>serS pfl serC</i> (20 min)		*	<i>uvrC tyrP flaD</i> (42 min)
4-14	65	5C10 (504), 6H4 (505), 17B2 (506)	7-19	6	8F9 (127), 8G4 (128), 5A5 (129), 3C7 (130)
	*	<i>pbpA</i> (2 min)		36	6A5 (314), 9A1 (315)
	*	<i>metC</i> (65 min)		*	<i>proA proB</i> (6 min)
4-15	50	9D2 (406), 12F12 (407), 2G11 (408)		*	<i>purA</i> (95 min)
4-20	36	20B5 (316), 6F11 (317)	7-39	35	7B6 (309)
4-21	40	9F2 (331), 7F2 (332), 6D1 (333), 12B3 (334)	7-42	69	18H7 (520), 14F11 (521), 7E3 (522)
	*	<i>fadD</i> (40 min)	7-47	56	6H2 (433), 7G4 (434), 4A12 (435)
4-23	22	4H11 (225), 2F1 (226), 5A12 (227)		*	<i>rnc lep</i> (55 min)
4-25	27	4D10 (247), 13H6 (248)	7-48	54	10H6 (425), 5A11 (426)
4-27	88	4H12 (539), 8B10 (540)		*	<i>purL</i> (55 min)
4-29	80	2C10 (577), 9B3 (578), 7C3 (579)	8-6	4	9H2 (117), 4E4 (118), 21C8 (119), 12D5 (120), E2B8 (121)
4-34	20	1E5 (212), 1H1 (213), 1F10 (214)		75	E4E4 (618)
	*	<i>gpt</i> (6 min)	8-9	30	2C3 (263), 4E7 (264)
4-35	90	7B7 (533)		*	<i>dnaC</i> (99 min)
4-39	41	20H4 (337)	8-12	13	23E10 (160), 12A1 (161), 2F5 (162)
	*	<i>dnaC aspS</i> (99 min)		*	<i>glpT</i> (49 min)
4-42	46	1H4 (357), 10H4 (358), 8F4 (359)	8-17	21	E1D1 (218), 11F5 (219)
4-43	4	15A7 (116), 9H2 (117), 4E4 (118)	8-24	49	20E7 (377), 22C4 (378), 4B4 (379)
	75	E4E4 (618)		*	<i>glpT</i> (49 min)
	*	<i>mrcB fhuACDB</i> (4 min)	8-25	12	6E7 (157)
4-44	11	19B7 (150), 8C4 (151)		*	<i>purE</i> (12 min)
	*	<i>mrcB fhuACDB</i> (4 min)	8-29	49	20E7 (377), 22C4 (378), 4B4 (379)
	*	<i>acrA</i> (11 min)	8-42	10	3B6 (148), 7E2 (149), 19B7 (150)
4-45	23	7B5 (228), 10E11 (229)		*	<i>cya</i> (85 min)
	*	<i>putP putA</i> (23 min)	8-47	95	1D4 (650), 3H6 (651), 3A1 (652)
	*	<i>proT</i> (83 min)		*	<i>psd</i> (95 min)
4-46	1	2F7 (104), 4A3 (105), 8D2 (106)	9-3	50	E9C9 (405), 9D2 (406)
	*	<i>folA</i> (1 min)	9-12	76	1B6 (613), 5B10 (614), 10F5 (615)
5-8	63	6C5 (472), 1H10 (473), 23G4S (474)		49	5H12 (380)
	*	<i>speAB endA metK</i> (63 min)	9-24	25	<i>livPGH</i> (76 min)
5-9	97	5C4 (659), E4D8 (660), 16H7S (661)		*	7F9 (239), 20E6 (240), 3E11 (241)
5-14	36	4H6 (318), 13H4 (319)		*	<i>pin</i> (26 min)
	*	<i>speAB endA metK</i> (63 min)	9-28	92	7A4 (633), 1F8 (634), 12B4 (635), 1E4 (636)
5-21	16	16A8 (171), 3A6 (172)		*	<i>dgkA plsB</i> (92 min)
5-23	4	21C8 (119)	9-34	70	3G10 (523), 8D6 (524)
	10	19F6 (146)		*	<i>pdxC</i> (20 min)
	25	20E6 (240)	9-44	25	7F9 (239), 20E6 (240), 3E11 (241)
	28	14C4 (252), 4F1 (253), 13F9 (254)	10-4	38	5E12 (327), 4B8 (328), 12H7 (329)
	59	25D2 (450)		*	<i>xthA</i> (38 min)
	*	<i>trpBCDE topA cysB</i> (28 min)	10-6	40	12B3 (334), 15D5 (335)
5-26	16	3A6 (172), 11A10 (173)	10-7	81	2A6 (572), 4D2 (573), 16B11 (574)
5-45	85	1C10 (551), 7G3 (552), 12G1 (553)		*	<i>rfa</i> (81 min)
6-2	11	8C4 (151), 12H5 (152)	10-9	81	17G2 (576), 2C10 (577), 9B3 (578)
	*	<i>dnaZ dnaX</i> (11 min)		16	3G6 (174)
6-5	13	2C4 (158), 8F11 (159), 23E10 (160)	10-15	80	9B3 (578), 7C3 (579), 10C8 (580), 6F2 (601)
6-7	22	4H11 (225), 2F1 (226), 5A12 (227)		*	<i>xyl</i> (80 min)
	*	<i>leuB</i> (2 min)	10-19	35	E3F2 (311), 11H12 (312), 6A3 (313), 6A5 (314)
6-12	22	4H11 (225), 2F1 (226), 5A12 (227)	10-24	11	*
6-13	25	20E6 (240), 3E11 (241)		*	<i>pnt</i> (35 min)
	*	<i>pin</i> (26 min)	10-25	25	8C4 (151), 12H5 (152)
6-16	54	10H6 (425), 5A11 (426), 8E3 (427)		*	<i>dnaZ</i> (11 min)
	*	<i>ftsB</i> (49 min)	10-26	47	7F9 (239), 20E6 (240), 3E11 (241)
	*	<i>purL</i> (55 min)		1E1 (363), 2B1 (364), 7F1 (365), 7H12 (366), 5H11 (367)	
6-19	35	12E2 (308), 7B6 (309), 6F6 (310), E3F2 (311)		11	8C4 (151), 12H5 (152)
6-24	22	4H11 (225), 2F1 (226), 5A12 (227)		*	<i>dnaZ</i> (11 min)
6-27	19	3H12 (209), 5F4 (210)		*	<i>mgIBAC</i> (45 min)
6-29	63	6C5 (472), 1H10 (473)		*	<i>putPA</i> (23 min)
6-32	4	15A7 (116), 9H2 (117), 4E4 (118), 21C8 (119), 12D5 (120), E2B8 (121)	10-29	23	7B5 (228), 10E11 (229)
	75	E4E4 (618)	10-30	27	4D10 (247), 13H6 (248)
	*	<i>dapC garB mrcB fhuACDB popC optA dapD glnD cds rpsB tsf</i> (4 min)	10-47	60	8B9 (455), 10B5 (456)
6-41	9	9G9 (144), 4F3 (145), 19F6 (146)	10-48	60	*
					eno (60 min)
					8B9 (455), 10B5 (456)

Continued on following page

TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^d	Kohara clones hybridized ^b and genes ^c
11-5	31	5F1 (266), 1A7 (267), 7F12 (268)	15-5	27	12A3 (246), 4D10 (247), 13H6 (248)
11-7	81	5D2 (575), 17G2 (576), 2C10 (577)		15	4A5 (166), 3G5 (167), 1G6 (168)
	*	<i>mtlCAD</i> (81 min)		*	<i>lip dacA envT rodA pbpA leuS</i> (15 min)
11-8	60	1B3 (454), 8B9 (455)	15-10	12	6E7 (157), 2C4 (158)
	*	<i>eno</i> (60 min)	15-16	12	6E7 (157), 2C4 (158)
11-9	92	1F8 (634), 12B4 (635), 1E4 (636), 12D1 (637)	15-17	40	7F2 (332), 6D1 (333), 12B3 (334)
	*	<i>dnaB</i> (92 min)		*	<i>fadD</i> (40 min)
11-10	65	21H2 (479), 3B2 (480), 8A5 (501), 2F9 (502)	15-18	88	4B6 (541), 7G8 (542), 6H5 (543)
	68	8F8 (514), 6B5 (515), 20F4 (516)		81	16B11 (574), 5D2 (575)
11-12	65	21H2 (479), 3B2 (480), 8A5 (501), 2F9 (502)	15-19	36	9A1 (315), 20B5 (316)
	68	8F8 (514), 6B5 (515), 20F4 (516)	15-20	76	10F5 (615), 16A5 (616), E5B4 (617)
11-15	24	E4H10S (233), E3G11 (234), 14C1 (235)	15-25	18	3D4 (202), 24F9 (203), 1B4 (204)
	69	E4G11S (519)		36	6A5 (314), 9A1 (315), 20B5 (316)
	*	<i>flaKXLYM</i> (24 min)	15-27	60	10B5 (456), 8C5 (457)
11-16	30	2C3 (263), 4E7 (264)	15-29	22	4H9 (224), 4H11 (225)
11-38	21	E1D1 (218), 11F5 (219)		24	14C1 (235)
	*	<i>gpsA</i> (81 min)		*	<i>gpsA</i> (81 min)
11-41	4	9H2 (117), 4E4 (118), 21C8 (119), 12D5 (120), E2B8 (121)	15-31	63	1A2 (471), 6C5 (472), 1H10 (473)
	75	E4E4 (618)		*	<i>fda pgk</i> (63 min)
	98	19H10 (664), 3F1 (665), 1D6 (666)	15-32	40	7F2 (332), 6D1 (333), 12B3 (334)
12-2	88	12E3 (538), 4H12 (539), 8B10 (540)		*	<i>fadD</i> (40 min)
12-13	44	3B12 (348), 2G4 (349), 6D9 (350)	15-33	93	12A6 (641), 10H5 (642), 12H2 (643)
12-15	3	15B8 (111), 4D12 (112)	15-36	55	8E12 (432), 6H2 (433)
12-21	25	7F9 (239), 20E6 (240)	15-37	66	6B12 (507), 9F9 (508)
12-34	4	21C8 (119)	15-41	36	6A5 (314), 9A1 (315), 20B5 (316)
	10	19F6 (146)	15-48	81	17G2 (576), 2C10 (577)
	28	14C4 (252), 4F1 (253)		*	<i>mtlCAD</i> (81 min)
	59	25D2 (450)		16-1	18C4 (629) .
	*	<i>trpABCDE</i> (28 min)		*	<i>rrnD aroE</i> (72 min)
12-48	18	3D4 (202), 24F9 (203), 1B4 (204)	16-4	88	4H12 (539), 8B10 (540)
13-1	11	4B10 (153), 7C12 (154), 8E4 (155)		*	<i>pfkA tpiA cpxA cdh</i> (88 min)
	32	8B7 (274), 6D4 (275)	16-7	72	18C4 (629)
13-2	90	E11C11 (534)	16-10	35	6F6 (310), E3F2 (311), 11H12 (312)
13-3	41	20H4 (337), 12C7 (338)	16-11	24	E4H10S (233), E3G11 (234)
13-12	51	6F7 (410), 3A11 (411)	16-25	95	<i>rrna</i> (87 min)
	*	<i>uvrC tyrP flaD</i> (42 min)		*	3A1 (652), 6G4 (653), 1G10 (654)
13-13	81	4D2 (573), 16B11 (574), 5D2 (575)	16-28	5	<i>purA</i> (95 min)
13-15	87	7G8 (542), 6H5 (543), 6H9 (544)	16-31	53	7D5 (125), 4A11 (126), 8F9 (127)
13-16	9	6E2 (141), 1A10 (142), 6A12 (143)	16-33	92	7A8 (422), 4C11 (423), 5A8 (424)
13-19	27	4D10 (247), 13H6 (248)		*	1F8 (634), 12B4 (635), 1E4 (636)
13-20	36	6F11 (317), 4H6 (318), 13H4 (319)	16-34	92	<i>dgkA plsB</i> (92 min)
13-26	88	4B6 (541), 7G8 (542), 6H5 (543)		97	1F8 (634), 12B4 (635), 1E4 (636)
	33	1G9 (277), 9B8 (278)		*	E4D8 (660), 16H7S (661), 7G7 (662)
13-27	27	12A3 (246), 4D10 (247), 13H6 (248)	16-37	94	<i>dgkA</i> (92 min)
	*	<i>metD</i> (5 min)		*	8H1 (645), 5H2 (646)
13-31	47	1E1 (363), 2B1 (364)	16-43	94	<i>melA</i> (93 min)
13-32	25	E9G1 (236), 15A8 (237)		*	9B1 (649), 1D4 (650), 3H6 (651)
13-42	74	4D4 (622), 6F9 (623), 15C3 (624), 4C5 (625)	16-44	55	<i>mopAB ampC frd</i> (94 min)
	*	<i>trpS dam</i> (74 min)	16-46	47	7F8 (429), 5E10 (430), 6F10 (431)
13-47	36	6F11 (317), 4H6 (318), 13H4 (319)	17-16	60	2B1 (364), 7F1 (365), 7H12 (366), 5H11 (367)
	*	<i>sodB</i> (36 min)		*	8C5 (457), 9A12 (458), 10B6 (459), 3G11 (460)
14-9	82	8E8 (567), 7C4 (568), 1D11 (569), 12D11 (570)	17-22	100	<i>argA</i> (61 min)
	*	<i>uhpTRA ilvB</i> (82 min)		*	12A4 (675), 15A5 (676), 9E4 (101)
14-12	49	20E7 (377), 22C4 (378)	17-24	81	<i>phoM cet dye fexA msp seg sfrA thr</i> (100 min)
	*	<i>glpT glpA</i> (49 min)		*	2A6 (572), 4D2 (573), 16B11 (574)
14-18	21	11F5 (219), 7F6 (220), 9E9 (221)	17-26	14	<i>rfa</i> (81 min)
14-26	72	18C4 (629)	17-27	85	2D12 (164), 25A7 (165), 4A5 (166)
14-28	86	10H11 (548), 9B11 (549), 16G1 (550), 1C10 (551)	17-28	85	7B1 (555), 2A8 (556), 2E6 (557)
	*	<i>sfrB</i> (86 min)		*	<i>sbaA</i> (97 min)
14-29	44	6D9 (350), 21H10 (351)	17-30	53	4C11 (423), 5A8 (424)
	*	<i>his argS</i> (44 min)		*	<i>dapA purC</i> (53 min)
14-33	28	18B6 (255)	17-32	3	4D12 (112), 4E11 (113)
14-37	1	2F7 (104), 4A3 (105), 8D2 (106)	17-38	94	8H1 (645), 5H2 (646), 21H11 (647), 5G7 (648)
	*	<i>trkC folA ksgA pdxA</i> (1 min)		*	<i>recA</i> (58 min)
14-48	37	8G8 (321), 20F5 (322)	17-43	58	<i>melAB bymA pheR lysU</i> (93 min)

Continued on following page

TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c
17-47	*	<i>recA srl</i> (58 min)	22-2	80	7C3 (579), 10C8 (580), 6F2 (601)
17-47	82	3D1 (566), 8E8 (567), 7C4 (568), 1D11 (569), 12D11 (570)	22-3	*	<i>dnaY</i> (13 min)
18-11	*	<i>uhpTRA ilvB</i> (82 min)	22-3	84	2A8 (556), 2E6 (557), 15D10 (558)
18-11	36	6F11 (317), 4H6 (318), 13H4 (319)	22-4	*	<i>kdsB ilvGEDA</i> (85 min)
18-28	*	<i>cfa sodB</i> (36 min)	22-4	0	15A5 (676), 9E4 (101), 6H3 (102)
18-28	66	6B12 (507), 9F9 (508)	22-5	*	<i>deoD</i> (99 min)
18-35	*	<i>dapE</i> (53 min)	22-5	57	E8F2 (438), 22D7 (439)
18-35	44	7D4 (346), 9B2 (347), 3B12 (348)	22-8	72	6G9 (530), 3C5 (531), 9B9 (532), 18C4 (629)
18-38	54	8E3 (427), 2D5 (428), 7F8 (429)	22-8	*	<i>dnaY</i> (13 min)
18-42	*	<i>argG dacB</i> (69 min)	22-10	*	<i>kdsB ilvGE</i> (85 min)
18-42	58	23B7 (446), 9G10 (447), 1B2 (448)	22-11	92	3F12 (638), 10G7 (639), 1A11 (640)
18-44	*	<i>recA srlCAD</i> (58 min)	22-11	70	7E3 (522), 3G10 (523)
18-44	35	12E2 (308), 7B6 (309)	22-36	*	<i>rrnD aroE</i> (72 min)
18-45	35	E3F2 (311), 11H12 (312), 6A3 (313)	22-36	45	10A9 (353), 7A3 (354), 2E1 (355), 3G4 (356)
19-3	8	9F1 (137), 10A6 (138)	22-40	*	<i>rrnC kdsB ilvGE</i> (85 min)
19-3	*	<i>rrnA</i> (87 min)	22-40	58	23B7 (446), 9G10 (447)
19-5	81	16B11 (574), 5D2 (575)	22-45	*	<i>recA srl</i> (58 min)
19-11	81	16B11 (574), 5D2 (575)	22-45	50	E9C9 (405), 9D2 (406), 12F12 (407)
19-11	*	<i>cysE</i> (81 min)	22-46	30	4E7 (264), 10E6 (265), 5F1 (266)
19-19	3	11C5 (115), 15A7 (116), 9H2 (117)	22-46	21	E1D1 (218), 11F5 (219)
19-19	*	<i>mrcB fhuACDB</i> (4 min)	22-48	4	21C8 (119)
19-24	49	E13A5 (376), 20E7 (377), 22C4 (378), 4B4 (379)	22-48	10	19F6 (146)
19-32	*	<i>nrdAB ftsB glpQT</i> (48 min)	22-48	28	4F1 (253), 13F9 (254), 18B6 (255)
19-32	12	8E4 (155), 9E5 (156)	23-3	59	59
19-36	20	1F10 (214), E6H3 (215), 13E3 (216)	23-3	54	25D2 (450)
19-38	44	3B12 (348), 2G4 (349)	23-3	*	<i>recA</i> (58 min)
19-39	12	8F4 (155), 9E5 (156)	23-3	*	5A11 (426), 8E3 (427), 2D5 (428)
19-39	61	5A10 (461), 8H3 (462), 12H3 (463)	23-3	*	<i>guaAB</i> (54 min)
19-48	3	4D12 (112), 4E11 (113)	23-3	*	<i>ilvEDAYC hemD rep trxA rho gpp bfm cya</i> (85 min)
19-48	*	<i>ftsE</i> (76 min)	23-4	54	5A11 (426), 8E3 (427), 2D5 (428)
20-5	64	23G4S (474), 12C6 (475), 3A9 (476), 3D11 (477)	23-4	55	12E2 (308), 7B6 (309)
20-5	*	<i>speC</i> (64 min)	23-4	21	E1D1 (218), 11F5 (219), 7F6 (220), 9E9 (221)
20-10	89	4G11 (535), 8H10 (536), 6D8 (537)	23-4	*	<i>asnS</i> (21 min)
20-17	*	<i>ppc argE argCBH</i> (89 min)	23-4	0	15A5 (676), 9E4 (101), 6H3 (102)
20-23	50	12F12 (407), 2G11 (408), 2C9 (409)	23-4	69	18H7 (520), 14F11 (521)
20-25	83	2A2 (563), 3F11 (564), 3C10 (565), 3D1 (566)	23-4	*	<i>nusA argG</i> (69 min)
20-25	46	3E4 (360), 2B4 (361), 17A4 (362)	23-4	58	23B7 (446), 9G10 (447), 1B2 (448)
20-25	11	7C12 (154)	23-4	*	<i>recA</i> (58 min)
20-28	*	<i>metG</i> (46 min)	23-4	90	9B9 (532)
20-28	43	3B3 (343), 25D8 (344)	23-4	*	<i>rrnG</i> (56 min)
20-30	8	10A6 (138), 7H10 (139), 8F10 (140)	23-4	35	8D1 (672), 5C1 (673), 15C9 (674)
20-30	*	<i>lacYZ lacI</i> (8 min)	23-4	21	12E2 (308), 7B6 (309)
20-33	22	E2E5 (222), 9B10 (223)	23-4	*	E1D1 (218), 11F5 (219), 7F6 (220), 9E9 (221)
20-37	37	15G10 (320), 8G8 (321)	23-4	99	<i>–</i> (99 min)
20-39	3	4D12 (112), 4E11 (113), 17C11 (114)	23-4	99	8D1 (672), 5C1 (673), 15C9 (674)
20-46	54	2D5 (428), 7F8 (429), 5E10 (430)	23-4	*	<i>–</i> (99 min)
21-2	41	20H4 (337), 12C7 (338)	23-4	41	20H4 (337), 12C7 (338)
21-2	*	<i>flaHG cheZYBR</i> (41 min)	23-4	*	<i>args flaHG cheZYB</i> (41 min)
21-10	84	2E6 (557), 15D10 (558)	23-4	58	23B7 (446), 9G10 (447), 1B2 (448)
21-11	41	20H4 (337)	23-4	*	<i>flaD hag flbC flaN</i> (42 min)
21-11	*	<i>argG</i> (69 min)	23-4	54	8E3 (427), 2D5 (428), 7F8 (429)
21-15	19	4H6 (211)	23-4	22	9E9 (221), E2E5 (222)
21-21	69	18H7 (520), 14F11 (521)	23-4	*	<i>rrn</i> (–)
21-33	58	23B7 (446), 9G10 (447)	23-4	58	23B7 (446), 9G10 (447), 1B2 (448)
21-33	*	<i>recA srl</i> (58 min)	23-4	*	<i>recA</i> (58 min)
21-35	84	2A8 (556), 2E6 (557), 15D10 (558)	23-4	58	23B7 (446), 9G10 (447), 1B2 (448)
21-35	*	<i>kdsB ilvGEDA</i> (85 min)	23-4	*	<i>adk</i> (11 min)
21-40	57	E8F2 (438), 22D7 (439), 24G1 (440), 4C9 (441)	23-4	58	23B7 (446), 9G10 (447), 1B2 (448)
21-40	*	<i>recA</i> (58 min)	23-4	*	<i>recA srl</i> (58 min)
21-42	61	8H3 (462), 12H3 (463)	23-4	50	12F12 (407), 2G11 (408)
21-43	93	2C12 (644), 8H1 (645), 5H2 (646)	23-4	11	7C12 (154)
21-44	97	16H7S (661), 7G7 (662)	23-4	46	8F4 (359), 3E4 (360)
22-1	12	2C4 (158), 8F11 (159)	23-4	23	7B5 (228), 10E11 (229), 9G7 (230)
22-1	*	<i>dnaY</i> (13 min)	23-4	24	E4H10S (233), E3G11 (234), 14C1 (235)

Continued on following page

TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^d	Kohara clones hybridized ^b and genes ^c
25-5	47	1E1 (363), 2B1 (364), 7F1 (365)	28-32	*	<i>adk</i> (11 min)
25-8	99	10H12 (670), 7C1 (671), 8D1 (672), 5C1 (673)	28-32	77	4D9 (607), 12E4 (608)
	*	<i>dnaC</i> (99 min)	28-32	*	<i>adk</i> (11 min)
25-14	53	4C11 (423), 5A8 (424), 10H6 (425)	28-33	92	1E4 (636), 12D1 (637)
	73	E1H9 (628)	28-33	*	<i>proA</i> (6 min)
	*	<i>purC</i> (53 min)	28-33	*	<i>tyrB</i> (92 min)
25-18	98	5G8 (667), 8H8 (668), 12G5 (669)	28-34	7	5E5 (132), 3E3 (133), 9G4 (134)
	*	<i>pyrC</i> (23 min)	28-36	87	9H1 (545), 10F1 (546), 8D12 (547)
25-23	18	4H7 (201), 3D4 (202), 24F9 (203)	28-44	50	9D2 (406), 12F12 (407)
	*	<i>bioABFCD uvrB</i> (18 min)	28-44	*	<i>hisJP purF pdxB hisT</i> (50 min)
25-25	85	12G1 (553), 10F4 (554)	28-47	89	12E3 (538), 4H12 (539)
	*	<i>proA prob</i> (6 min)	28-48	36	6A5 (314), 9A1 (315), 20B5 (316)
	*	<i>leuT hisR</i> , two other tRNA genes (84 min)	28-48	*	<i>nth</i> (-)
25-31	85	12G1 (553), 10F4 (554)	29-1	18	4C6 (206), 3E5 (207), 1E2 (208), 3H12 (209)
25-33	94	2C12 (644), 8H1 (645), 5H2 (646), 21H11 (647)	29-5	85	1C10 (551), 7G3 (552), 12G1 (553)
	*	<i>melAB</i> (93 min)	29-5	*	<i>ilvAYC hemD rep trxA rho gpp bfm cya dnap uvrD</i> (85 min)
25-35	84	4F4 (559), 2A1 (560), 7A1 (561)	29-15	22	E2E5 (222), 9B10 (223)
25-39	28	4F1 (253), 13F9 (254)	29-15	98	9H9 (663), 19H10 (664)
	4	21C8 (119)	29-15	*	<i>fabA</i> (22 min)
	10	19F6 (146)	29-39	63	1A2 (471), 6C5 (472)
	59	25D2 (450)	29-41	28	14C4 (252), 4F1 (253), 13F9 (254)
26-3	84	2A8 (556), 2E6 (557)	29-41	4	21C8 (119)
	*	<i>kdsB ilvGEDA</i> (85 min)	29-41	10	19F6 (146)
26-4	3	15B8 (111), 4D12 (112)	29-41	59	25D2 (450)
26-5	51	2C9 (409), 6F7 (410), 3A11 (411)	29-43	*	<i>trpCDE</i> (28 min)
	*	<i>fadL</i> (51 min)	29-43	4	21C8 (119), 12D5 (120)
26-6	2	6C1 (109), 6F3 (110), 15B8 (111)	29-47	74	1C9 (621), 4D4 (622), 6F9 (623)
	*	<i>leuA ilvIH mafB serR arl polB mraAB ppbB murE murF</i> (2 min)	29-47	*	<i>aroB mrcA</i> (75 min)
26-8	38	5E12 (327), 4B8 (328)	30-1	54	5A11 (426), 8E3 (427), 2D5 (428), 7F8 (429)
	*	<i>xthA</i> (38 min)	30-3	11	8C4 (151), 12H5 (152)
26-13	27	12A3 (246), 4D10 (247), 13H6 (248)	30-3	*	<i>apt dnaZ dnaX</i> (11 min)
26-17	17	25C10S (175), 7E10 (176)	30-4	11	8C4 (151), 12H5 (152)
	*	<i>glnS gltA sdh</i> (16 min)	30-4	*	<i>dnaZ dnaX</i> (11 min)
26-19	4	11C5 (115), 15A7 (116), 9H2 (117), 4E4 (118)	30-6	18	24F9 (203)
26-22	96	E1F5 (658), 5C4 (659)	30-6	10	4F3 (145), 19F6 (146), 2H5 (147)
	*	<i>pyrB argI sbaA valS</i> (97 min)	30-15	34	1F9 (304), 2H2 (305), 2B2 (306), 9E12 (307)
26-23	50	12F12 (407), 2G11 (408), 2C9 (409)	30-15	*	<i>adk</i> (11 min)
	*	<i>fabB</i> (50 min)	30-15	*	<i>ilvEDAYC</i> (85 min)
26-24	35	E3F2 (311), 11H12 (312), 6A3 (313)	30-16	9	8F10 (140), 6E2 (141)
	*	<i>pnt</i> (35 min)	30-17	14	25A7 (165), 4A5 (166), 3G5 (167), 1G6 (168)
26-30	18	10A8 (205), 4C6 (206), 3E5 (207)	30-17	84	2A8 (556), 2E6 (557), 15D10 (558)
	*	<i>tyrA</i> (57 min)	30-18	*	<i>ilvEDAYC hemD rep trxA rho</i> (85 min)
26-31	30	4A6 (262), 4E7 (264), 10E6 (265)	30-18	14	25A7 (165), 4A5 (166), 3G5 (167), 1G6 (168)
26-32	75	2F6 (620), 1C9 (621), 4D4 (622)	30-20	58	23B7 (446), 9G10 (447)
26-43	5	E2B8 (121), 6F5 (122), 10F9 (123)	30-20	*	<i>recA</i> (58 min)
	*	<i>pgsB firA acrC sefA dnaE</i> (4 min)	30-23	11	8C4 (151), 12H5 (152)
26-46	53	E8E3 (420), 4E10 (421), 7A8 (422)	30-23	*	<i>dnaZ dnaX</i> (11 min)
26-48	5	6F5 (122), 10F9 (123), 8G3 (124)	30-24	99	7C1 (671), 8D1 (672), 5C1 (673)
27-10	63	22H4 (468), 5E11 (469), 10B4 (470)	30-24	*	<i>dnaC</i> (99 min)
27-15	84	2A8 (556), 2E6 (557), 15D10 (558)	30-30	26	4D1 (242), 2A3 (243), 11G8 (244)
	*	<i>kdsB ilvGEDA</i> (85 min)	30-32	40	7F2 (332), 6D1 (333), 12B3 (334)
27-17	24	1H7 (232), E4H10S (233)	30-32	*	<i>fadD</i> (40 min)
27-18	17	25C10S (175), 7E10 (176)	30-34	27	12A3 (246), 4D10 (247)
	*	<i>glnS gltA sdh</i> (16 min)	30-39	40	7F2 (332), 6D1 (333), 12B3 (334)
27-35	35	6F6 (310), E3F2 (311), 11H12 (312)	30-42	34	1F9 (304), 2H2 (305), 2B2 (306), 9E12 (307)
	*	<i>pnt</i> (35 min)	30-43	88	12E3 (538), 4H12 (539), 8B10 (540)
27-37	63	6C5 (472), 1H10 (473), 23G4S (474)	30-43	*	<i>pfkA</i> (88 min)
	*	<i>speAB endA meiK</i> (63 min)	30-46	87	6H5 (543), 6H9 (544)
28-5	99	7C1 (671), 8D1 (672), 5C1 (673)	30-46	75	E5B4 (617), E3C10 (619), 2F6 (620)
	*	<i>dnaC</i> (99 min)	30-48	*	<i>glyS</i> (80 min)
28-6	73	3F8 (626), 9H3 (627)	31-5	37	8G8 (321), 20F5 (322)
28-8	9	6E2 (141), 1A10 (142), 6A12 (143)	31-6	43	25D8 (344)
28-25	1	8D2 (106), 5H5 (107)	31-16	76	7H7 (612), 1B6 (613), 5B10 (614)
28-27	7	5E5 (132), 3E3 (133), 9G4 (134)	31-16	*	<i>livK livL livJ htpR fam ftsE</i> (76 min)
28-31	54	10H6 (425), 5A11 (426), 8E3 (427), 2D5 (428)	31-31	69	16C4 (517), 13A9 (518)

Continued on following page

TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c
31-32	76	7H7 (612), 1B6 (613), 5B10 (614)	34-46	28	4F1 (253), 13F9 (254)
	*	<i>livK livL livJ htpR fam ftsE</i> (76 min)		54	4A12 (435), 3F10 (436), 21D7 (437)
31-38	21	7F6 (220), 9E9 (221), E2E5 (222)		4	21C8 (119)
	*	<i>pyrD</i> (21 min)		10	19F6 (146)
31-39	99	12G5 (669), 10H12 (670), 7C1 (671), 8D1 (672)		59	25D2 (450)
	*	<i>dnaC</i> (99 min)		*	<i>nadB trmC ranA ung pss</i> (56 min)
32-1	61	9A12 (458), 10B6 (459), 3G11 (460)	34-47	28	4F1 (253), 13F9 (254)
32-9	80	10C8 (580), 6F2 (601)		4	21C8 (119)
	*	<i>xyl</i> (80 min)		10	19F6 (146)
32-10	92	1F8 (634), 12B4 (635), 1E4 (636)		59	25D2 (450)
	*	<i>dgkA plsB</i> (92 min)	35-1	55	7F8 (429), 5E10 (430)
	*	<i>serB ftrA trpR phoM</i> (100 min)		28	14C4 (252), 4F1 (253)
32-12	28	14C4 (252), 4F1 (253), 13F9 (254)		*	<i>trpR phoM cet dye fexA msp seg sfrA thr</i> (100 min)
	4	21C8 (119)	35-2	98	9H9 (663), 19H10 (664), 3F1 (665), 1D6 (666)
	10	19F6 (146)	35-3	7	3E3 (133), 9G4 (134)
	59	25D2 (450)	35-4	82	8E8 (567), 7C4 (568), 1D11 (569)
	*	<i>trpABCDE</i> (28 min)		*	<i>uhpTRA ilvB</i> (82 min)
32-15	26	4D1 (242), 2A3 (243), 11G8 (244)	35-6	2	6C1 (109), 6F3 (110)
32-19	35	12E2 (308), 7B6 (309)	35-7	55	7F8 (429), 5E10 (430), 6F10 (431)
32-27	28	14C4 (252), 4F1 (253), 13F9 (254)	35-25	19	3H12 (209)
	4	21C8 (119)	35-30	43	9G6 (345), 7D4 (346)
	10	19F6 (146)	35-38	23	7B5 (228), 10E11 (229)
	59	25D2 (450)		*	<i>putP</i> (23 min)
	*	<i>trpABCDE</i> (28 min)		*	<i>prot</i> (83 min)
32-38	70	7C8 (525), 1E3 (526), 3G9 (527)	36-11	24	E4H10S (233), E3G11 (234), 14C1 (235)
	*	<i>argR</i> (71 min)		69	E4G11S (519)
32-45	54	5A8 (424), 10H6 (425), 5A11 (426)		96	E1F5 (658)
32-46	85	12G1 (553), 10F4 (554)	36-28	84	<i>flaVKXLYM</i> (24 min)
	6	5A5 (129), 3C7 (130)		84	2A1 (560), 7A1 (561)
	*	<i>proAB</i> (6 min)	36-35	84	2A1 (560), 7A1 (561)
32-48	24	1H7 (232), E4H10S (233)	37-2	59	9G10 (447), 1B2 (448), 12F2 (449)
	69	E4G11S (519)	37-4	20	13E3 (216), 6D12 (217)
33-1	50	12F12 (407), 2G11 (408), 2C9 (409)	37-5	*	<i>pdxC aroA himD rpsA</i> (20 min)
	*	<i>fabB</i> (50 min)		91	6G10 (631), 4E5 (632), 7A4 (633)
33-4	42	16B12 (341), 4B9 (342)		4	4E4 (118)
33-5	63	1A2 (471), 6C5 (472), 1H10 (473)		*	<i>pgi</i> (91 min)
	*	<i>fda pgk</i> (63 min)	37-6	49	20E7 (377), 22C4 (378)
33-10	85	10F4 (554), 7B1 (555), 2A8 (556), 2E6 (557)	37-11	55	2D5 (428), 7F8 (429), 5E10 (430), 6F10 (431)
33-14	60	10B5 (456), 8C5 (457), 9A12 (458)	37-16	81	16B11 (574), 5D2 (575)
33-15	44	6D9 (350), 21H10 (351)	37-24	36	6A5 (314), 9A1 (315), 20B5 (316)
33-18	25	E4C2 (238)		49	4B4 (379), 5H12 (380)
	63	1A2 (471), 6C5 (472), 1H10 (473)		*	<i>metC</i> (65 min)
	*	<i>purE</i> (12 min)	37-27	19	1E2 (208), 3H12 (209), 5F4 (210)
33-20	60	10B5 (456), 8C5 (457), 9A12 (458)	37-29	3	4D12 (112), 4E11 (113), 17C11 (114), 11C5 (115)
33-31	95	3H6 (651)		*	<i>speD</i> (3 min)
33-43	3	15B8 (111), 4D12 (112)	37-40	3	15B8 (111), 4D12 (112)
33-44	3	15B8 (111), 4D12 (112)		*	<i>guaC nadC lrs aroP ace</i> (3 min)
33-45	32	5F11 (273), 8B7 (274), 6D4 (275), 1G4 (276)	37-44	41	19H3 (336)
34-4	33	22E3 (280), 6E8 (301), 2A9 (302)	37-46	68	<i>eda edd</i> (41 min)
	69	18H7 (520), 14F11 (521)		*	15B3 (512), 21D1 (513)
	*	<i>nusA argG</i> (69 min)		*	<i>exuT</i> (68 min)
34-7	17	18F11 (177), 10G5 (178)	38-4	41	20H4 (337), 12C7 (338)
34-9	95	3A1 (652), 6G4 (653), 1G10 (654)	38-5	3	11C5 (115), 15A7 (116)
	*	<i>guaAB</i> (54 min)	38-15	1	8D2 (106), 5H5 (107), 8H11 (108)
	*	<i>purA</i> (95 min)	38-20	97	5C4 (659), E4D8 (660)
34-10	54	5A11 (426), 8E3 (427)	38-27	47	7F1 (365), 7H12 (366), 5H11 (367), 4F2 (368)
	*	<i>guaAB</i> (54 min)	38-39	4	9H2 (117), 4E4 (118), 21C8 (119), 12D5 (120), E2B8 (121)
34-13	52	12G2 (418), 5F7 (419), E8E3 (420)		75	E4E4 (618)
34-14	59	12F2 (449)		*	<i>dapD glnD cds rpsB tsf</i> (4 min)
34-20	5	E2B8 (121), 6F5 (122), 10F9 (123)	38-40	6	8G4 (128), 5A5 (129)
	*	<i>dnaE tdi pyrH metD proS fadE strC rrnH rrnH alaV ileV rrlH rrfH aspU dnaQ</i> (4 min)	38-41	85	7G3 (552), 12G1 (553)
34-26	70	7C8 (525), 1E3 (526)	38-43	90	7B7 (533)
34-27	82	12D11 (570), 7F3 (571), 2A6 (572), 4D2 (573)	39-5	47	1E1 (363), 2B1 (364), 7F1 (365)
34-30	59	12F2 (449)	39-16	50	12F12 (407), 2G11 (408), 2C9 (409)
34-43	82	8E8 (567), 7C4 (568), 1D11 (569)			
	*	<i>uhpRA ilvB</i> (82 min)			

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TABLE 1—Continued

pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c	pLC plasmid	Map position (min) ^a	Kohara clones hybridized ^b and genes ^c
39-31	55	* <i>fabB</i> (50 min) 8E12 (432), 6H2 (433), 7G4 (434)	43-2	35	* <i>nrdB ftsB glpQT</i> (48 min) 7B6 (309)
39-37	55	2D5 (428), 7F8 (429), 5E10 (430), 6F10 (431)	43-6	20	E6H3 (215), 13E3 (216), 6D12 (217)
39-45	19	3H12 (209), 5F4 (210), 4H6 (211)	43-25	21	7F6 (220), 9E9 (221), E2E5 (222)
40-5	20	E6H3 (215), 13E3 (216), 6D12 (217)	*	*	<i>pyrD</i> (21 min)
40-6	68	15B3 (512), 21D1 (513)	*	*	<i>uxuR uxuBA</i> (98 min)
40-24	95	3A1 (652), 6G4 (653), 1G10 (654)	43-31	13	12A1 (161), 2F5 (162), 21A9S (163), 2D12 (164)
40-27	8	7H10 (139), 8F10 (140)	43-32	53	4C11 (423), 5A8 (424)
40-33	34	2H2 (305), 2B2 (306), 9E12 (307)	73	E1H9 (628)	
40-33	82	7C4 (568), 1D11 (569), 12D11 (570)	*	*	<i>purC</i> (53 min)
40-33	*	<i>uhpT</i> (82 min)	43-46	94	21H11 (647), 5G7 (648), 9B1 (649), 1D4 (650), 3H6 (651)
40-42	31	7F12 (268), 3C9 (269), 24D6 (270), 1A6 (271)	*	*	<i>mopAB ampC frdDCBA</i> (94 min)
40-43	28	18B6 (255), E14F6 (256), 1C2 (257)	43-47	66	6H4 (505), 17B2 (506), 6B12 (507)
40-43	8	7H10 (139), 8F10 (140)	44-2	11	7E2 (149), 19B7 (150), 8C4 (151)
40-44	80	9B3 (578), 7C3 (579), 10C8 (580)	44-5	11	7E2 (149), 19B7 (150), 8C4 (151)
41-4	85	12G1 (553), 10F4 (554)	44-7	84	7B1 (555), 2A8 (556), 2E6 (557), 15D10 (558)
41-4	*	<i>ilvDAYC hemD rep trxA rho gpp bfm cya dnaP uvrD</i> (85 min)	*	*	<i>ilvGEDAYC hemD rep trxA rho gpp bfm cya</i> (85 min)
41-7	55	5E10 (430), 6F10 (431), 8E12 (432)	44-11	6	8F9 (127), 8G4 (128), 5A5 (129), 3C7 (130)
41-7	*	<i>flaN flaBCOE flaARQP</i> (43 min)	*	*	<i>gpt phoE proAB</i> (6 min)
41-11	6	4A11 (126), 8F9 (127), 8G4 (128)	44-12	11	2H5 (147), 7E2 (149), 19B7 (150), 8C4 (151)
41-13	40	12B3 (334), 15D5 (335)	44-13	95	3H6 (651), 3A1 (652)
41-13	89	4G11 (535), 8H10 (536)	44-14	92	*
41-15	*	<i>argH trmA</i> (89 min)	44-14	*	<i>ubiAC dinF lexA tnm dnaB dgkA plsB tyrB uvrA</i> (92 min)
41-15	28	14C4 (252), 4F1 (253), 13F9 (254)	44-22	79	10C8 (580), 6F2 (601), 9F6 (602)
41-15	4	21C8 (119)	*	*	<i>xyl</i> (80 min)
41-15	10	19F6 (146)	44-23	84	2A1 (560), 7A1 (561)
41-15	59	25D2 (450)	44-24	36	6A5 (314), 9A1 (315), 20B5 (316)
41-15	*	<i>trpCDE topA cysB</i> (28 min)	44-25	19	3H12 (209), 5F4 (210)
41-24	25	7F9 (239), 20E6 (240), 3E11 (241)	44-36	36	6A5 (314), 9A1 (315), 20B5 (316)
41-30	7	3E3 (133), 9G4 (134), 6E6 (135)	44-41	36	6A5 (314), 9A1 (315), 20B5 (316)
41-33	97	E1F5 (658), 5C4 (659), E4D8 (660)	*	*	<i>mopB</i> (94 min)
41-34	41	20H4 (337)	*	*	<i>rpsF</i> (95 min)
41-37	99	8D1 (672), 5C1 (673), 15C9 (674)	44-47	36	6A5 (314), 9A1 (315), 20B5 (316)
41-40	55	7F8 (429), 5E10 (430), 6F10 (431)			
41-47	92	3F12 (638), 10G7 (639), 1A11 (640)			
42-13	63	5B4 (467), 22H4 (468), 5E11 (469)			
42-17	*	RF2 (-)			
42-17	49	20E7 (337), 22C4 (378)			

^a Approximate map location of pLC plasmids deduced from the hybridization data.^b The *E. coli* ordered clones that gave positive spots in the hybridization experiments (Fig. 1). The clone numbers as defined in the miniset (11) of *E. coli* ordered clone bank are shown in parentheses.^c Genes that were attributed to the plasmid by Phillips et al. (18) are shown on lines labeled with an asterisk in column 2. Their approximate map locations are shown in parentheses.

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